What is claimed is:

1. A system for characterizing cells present in an environment, the system comprising:

a) a collection device having a plurality of capillary microcosms for collecting or maintaining cells in the environment;

b) a sampling device for sampling cells present in the capillary microcosms; and

c) a characterizing device for characterizing the cells from the capillary microcosms;

wherein the sampling device is adapted to provide a plurality of samples to the characterizing device.

2. The system of claim 1, wherein the collection device comprises:

i) a housing;

ii) an array of capillary microcosms within the housing; and

iii) a fluid manifold in fluid communication with the capillary microcosms for controllably providing a cell-containing fluid from the environment to the capillary microcosms, wherein the housing comprises an opening to controllably permit cells from the environment to access the array.

3. The system of claim 2, wherein at least one of the capillary microcosms is provided with a substrate for trapping cells.

4. The system of claim 1, wherein the collection device further comprises a pump for pumping fluid into the fluid manifold.

5. The system of claim 1, wherein the collection device comprises at least one sensor for real-time monitoring of a condition within the collection device.

6. The system of claim 2, wherein the array of capillary microcosms is configured for use with an automated sampling device.

7. The system of claim 6, wherein the sampling device comprises an automated fluid handling device.

8. The system of claim 1, wherein the sampling device further comprises means for performing sample clean-up.

9. The system of claim 1, wherein the characterizing device comprises a mass spectrometer.

10. The system of claim 1, wherein the cells are selected from the group consisting of prokaryoyes, eukaryotes, yeasts, fungi, bacteria, Archaea, parasites, protozoa, plant cells, and animal cells.

11. A method for characterizing cells in an environment, the method comprising:

a) placing a collecting device in the environment to collect microorganisms, the collecting device comprising:

i) an array of capillary microcosms for trapping cells; and

ii) a housing surrounding the array and having an opening to controllably permit cells from the environment to access the array;

b) retrieving the collecting device from the environment;

c) sampling at least one of the capillary microcosms to obtain at least one sample;

d) analyzing the at least one sample to characterize the cells in the environment.

12. The method of claim 11, wherein the step of sampling comprises using an automated sample handling device.

13. The method of claim 12, wherein the step of sampling at least one of the microcosms comprises:

a) obtaining the at least one sample using an automated sample handling device; and

b) concentrating the at least one sample for analysis.

14. The method of claim 13, wherein the step of analyzing comprises analysis by mass spectrometry.

15. The method of claim 14, wherein the step of analyzing comprises using MALDI TOF mass spectrometry to characterize the cells.

16. The method of claim 15, wherein the cells are characterized as whole cells.

17. The method of claim 15, wherein a cell lysate is analyzed using MALDI TOF.

18. The method of claim 14, wherein the step of analyzing further comprises comparing at least one molecular weight determined by mass spectrometry to a computerized library of molecular weights.

19. The method of claim 15, wherein the cells comprise a microorganism useful for bioremediation.

20. The method of claim 15, wherein the cell comprises *Sphingomonas wittichii* Strain RW1.

21. The method of claim 14, wherein the step of analyzing by mass spectrometry comprises analyzing an isotopically labeled molecule.

22. The method of claim 14, wherein the step of analyzing comprises determining a turnover rate of a compound of interest.

23. A method for optimizing medical treatment for a patient, the method comprising:

a) providing a device comprising a housing and an array of capillary microcosms, each of the capillary microcosms being in fluid communication with a fluid manifold, and each of the capillary chambers containing either i) a case sample associated with a disease state of the patient or ii) a control sample;

b) subjecting each of said case and control samples to a treatment condition;

c) determining the effect of the treatment condition on each sample; and

d) selecting an optimized medical treatment for the patient.

24. The method of claim 23, wherein the treatment condition comprises treatment with a candidate pharmaceutical agent.

25. The method of claim 23, wherein the control sample is a sample of normal tissue from the patient.

26. The method of claim 23, wherein the case sample is a sample of diseased tissue from the patient.

27. A method for screening medical treatments for a patient, the method comprising:

a) providing a device comprising a housing and an array of test chambers, each of the test chambers being in fluid communication with a fluid manifold, and each of the test chambers containing either i) a candidate pharmaceutical agent or ii) a control;

b) exposing each of said test chambers to a biological fluid of the patient; and

c) determining the effect of the candidate pharmaceutical agent on the biological fluid.

28. The method of claim 27, further comprising:

d) selecting an optimized medical treatment for the patient.

29. The method of claim 27, wherein the candidate pharmaceutical agent comprises an antibiotic, an antineoplastic agent, an antidiabetic agent, an

anticoagulant agent, or a natural or synthetic nucleotide, polynucleotide, nucleotide mimetic, or polynucleotide mimetic.

30. The method of claim 29, wherein the biological fluid is blood.

31. The method of claim 27, wherein the device is implanted within the body of the patient.

32. The method of claim 27, wherein the step of determining the effect of the candidate pharmaceutical agent on the biological fluid comprises determining the bioavailability, biodistribution, or metabolism of the candidate pharmaceutical agent in the biological fluid.

33. The method of claim 27, wherein the step of determining the effect of the candidate pharmaceutical agent on the biological fluid comprises determining the antibiotic effect of a candidate pharmaceutical agent on a blood-borne pathogen.

34. A method for diagnosing an infectious or parasitic disease condition, the method comprising:

a) providing a device comprising a housing and an array of test chambers, each of the test chambers being in fluid communication with a fluid manifold and being configured to trap an infectious microorganism or parasite;

b) exposing each of said test chambers to a biological fluid of the patient;

c) identifying a microorganism or parasite trapped in a test chamber.

35. The method of claim 34, wherein the step of identifying comprises identifying a protein characteristic of the microorganism or parasite.

36. The method of claim 34, wherein the protein is identified using mass spectrometry.

37. The method of claim 36, wherein the protein is identified using multidimensional mass spectrometry.

38. A method for testing an agent to determine an effect of the agent on a living organism, the method comprising:

a) providing a device comprising a housing and an array of capillary microcosms, each of the capillary microcosms being in fluid communication with a fluid manifold, and each of the capillary chambers containing either i) the agent to be tested or ii) a control;

b) subjecting each of said agent and control samples to a fluid environment representative of a living organism; and

c) determining the effect of the agent on the fluid environment.

39. A method for detecting in a sample a microorganism having a pre-determined phenotype, the method comprising the steps of:

a) selecting a biomarker for the pre-determined phenotype;

b) providing a sample for testing;

c) detecting by mass spectroscopy the presence or absence of the biomarker diagnostic of a microorganism having the pre-determined phenotype in the sample.

40. The method of claim 39, wherein the biomarker is an enzyme.

41. The method of claim 40, wherein the enzyme is an oxygenase enzyme.

42. The method of claim 41, wherein the oxygenase is a dioxygenase.

43. The method of claim 39, wherein the step of detecting by mass spectroscopy comprises detecting an enzyme by peptide-mass fingerprinting.

44. The method of claim 43, wherein the step of detecting is performed on a digest of whole cells.

45. The method of claim 39, wherein the pre-determined phenotype is a phenotype useful for bioremediation.

46. The method of claim 39, wherein the microorganism is *Sphingomonas wittichii* Strain RW1.

47. The method of claim 39, wherein the microorganism is a parasite or pathogen.

48. The method of claim 39, comprising the further step of inducing biomarker production in the microorganism before detecting the presence or absence of the biomarker.

49. The method of claim 39, wherein the step of detecting by mass spectroscopy comprises detecting an enzyme by peptide sequencing using multi-dimensional mass spectrometry.